GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:07:01 ; Search time 755.06 Seconds
(without alignments)
27.251 Million cell updates/sec

Title: US-09-851-670-16
Perfect score: 24
Sequence: 1 gtccaaggcagagcaatttctgca 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	15.2	63.3	50	10	AAN91970	Complementary sequ
2	15	62.5	47	21	AAZ67988	Human map-related
c 3	14.6	60.8	27	22	AAC88881	HBV polyA sequence
4	14.6	60.8	47	21	AAZ67225	Human map-related
5	14.6	60.8	60	13	AAQ23683	PND EEE6405-1. Hu
6	14.2	59.2	44	20	AAX29732	Oligo #3 for scorp
c 7	14	58.3	50	21	AAZ87595	GM-CSF coding sequ
8	13.8	57.5	20	20	AAZ04797	PCR primer used to
9	13.8	57.5	23	20	AAV83732	PCR primer L for t
10	13.8	57.5	23	21	AAC65579	Uteroglobin knocko
11	13.8	57.5	23	21	AAZ58235	Mouse uteroglobin
12	13.6	56.7	26	20	AAX32801	Human mpl ligand a
c 13	13.6	56.7	26	20	AAX32802	Human mpl ligand a
14	13.6	56.7	47	21	AAZ69023	Human map-related
c 15	13.6	56.7	48	21	AAA53746	Str1 promoter RV r
16	13.4	55.8	34	22	AAH49705	Human PEP-utilisin
c 17	13.4	55.8	41	18	AAT78336	Chimeric virus con
c 18	13.4	55.8	41	22	AAH49707	Human PEP-utilisin
19	13.4	55.8	45	18	AAT78337	Chimeric virus con
20	13.4	55.8	51	21	AAA76892	Human clone cg3953
c 21	13.2	55.0	18	20	AAX33759	DNA tandem nucleot
c 22	13.2	55.0	18	20	AAX33731	DNA tandem nucleot
c 23	13.2	55.0	19	21	AAZ76916	Human biallelic ma
24	13.2	55.0	19	21	AAA84110	Cyclin C ribozyme
25	13.2	55.0	19	22	AAH59272	Cyclin C ribozyme
26	13.2	55.0	20	20	AAZ03580	PCR primer used to
27	13.2	55.0	20	20	AAZ01547	PCR primer used to
c 28	13.2	55.0	20	22	AAF33164	Human B7-1 antisen
29	13.2	55.0	23	22	AAH01931	blaTEM resistance
30	13.2	55.0	29	22	AAC81665	Human CD80 PCR pri
c 31	13.2	55.0	30	18	AAT96365	Primer IG-4 for so
c 32	13.2	55.0	31	21	AAA78908	Human genomic DNA
c 33	13.2	55.0	39	13	AAQ20917	PCR primer for amp
c 34	13.2	55.0	39	14	AAQ35122	Reverse PCR primer
c 35	13.2	55.0	39	15	AAQ70454	Primer to generate
c 36	13.2	55.0	39	16	AAT08521	Reverse primer for
c 37	13.2	55.0	39	20	AAZ23178	Oncostatin M cDNA
c 38	13.2	55.0	39	20	AAZ29979	Reverse PCR primer
c 39	13.2	55.0	39	20	AAX26418	Reverse PCR primer
c 40	13.2	55.0	39	20	AAX26401	Reverse PCR primer
c 41	13.2	55.0	39	20	AAV83660	Reverse PCR primer
c 42	13.2	55.0	39	20	AAV69776	CD28Ig and B7Ig fu
c 43	13.2	55.0	45	18	AAV17337	Primer 96 used in
c 44	13.2	55.0	53	21	AAA59238	PCR primer for cDN
c 45	13	54.2	19	20	AAZ21253	Human CG1CE PCR pr

ALIGNMENTS

RESULT 1
AAN91970/c
ID AAN91970 standard; DNA; 50 BP.
XX
AC AAN91970;
XX
DT 13-APR-1990 (first entry)
XX
DE Complementary sequence of the Neisseria gonorrhoeae 7.2kb plasmid
DE combined with the xt1 capture sequence.
XX
KW Neisseria gonorrhoeae 7.2 kb plasmid; beta lactamase; capture sequence;
KW TEM-1NH assay; temkit2c.7.
XX
OS Neisseria gonorrhoeae.
XX
FH Key Location/Qualifiers
FT misc_feature 1..30
FT /*tag= a
FT /"probe"
FT misc_feature 31..50
FT /*tag= b
FT /"xt1 capture sequence"
XX
PN WO8903891-A.
XX
PD 05-MAY-1989.
XX
PF 14-OCT-1988; 88WO-US03644.
XX
PR 30-SEP-1988; 88US-0252638, US-109282.
XX
PA (CHIR-) CHIRON CORP.
XX

PI Urdea MS, Warner B, Running JA, Kolberg JA, Clyne JM;
PI Sanchez-Pescador R;
XX
DR WPI; 1989-150787/20.
XX
PT Nucleic acid multimer for hybridisation assays
PT - having single-stranded oligo-nucleotide units
PT capable of binding specifically to sequences of interest.
XX
PS Fig 10-3; ; 112pp; English.
XX
CC Partial nucleotide sequences of a capture sequence used in the TEM-1NH
CC assay. The probe (tag a) is complementary to the N. gonorrhoeae 7.2 kb
CC plasmid downstream of the coding region of beta lactamase. It is called
CC temkit2c.7.
XX
SQ Sequence 50 BP; 11 A; 6 C; 17 G; 16 T; 0 other;

Query Match 63.3%; Score 15.2; DB 10; Length 50;
Best Local Similarity 85.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tccaaggcagagcaatttct 21
|||||| | |||||||| |||
Db 40 TCCAAAGAAGAGCAATCTCT 21

RESULT 2
AAZ67988
ID AAZ67988 standard; DNA; 47 BP.
XX
AC AAZ67988;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:2335.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 3; Page 728; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 10 A; 2 C; 16 G; 19 T; 0 other;

Query Match 62.5%; Score 15; DB 21; Length 47;
Best Local Similarity 78.3%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 gtccaaggcagagcaatttctgc 23
|| |||| ||| |||||| |||
Db 22 gtttaaggaagaacaatttgtgc 44

RESULT 3
AAC88881/c
ID AAC88881 standard; DNA; 27 BP.
XX
AC AAC88881;
XX
DT 05-MAR-2001 (first entry)
XX
DE HBV polyA sequence PCR primer 270R.
XX
KW Hepatitis B virus; HBV; adenovirus type 35; Ad35; adenovirus type 5; Ad5;
KW gene delivery vehicle; gene therapy; PCR primer; ss.
XX
OS Hepatitis B virus.
XX
PN EP1054064-A1.
XX
PD 22-NOV-2000.
XX
PF 16-MAY-2000; 2000EP-0201738.
XX
PR 17-MAY-1999; 99EP-0201545.
XX
PA (INTR-) INTROGENE BV.
XX
PI Bout A, Vogels R, Havenga MJE;
XX
DR WPI; 2001-001097/01.
XX
PT Adenovirus derived gene delivery vehicles comprising at least one
PT element of adenovirus type 35, efficiently transfers genetic material
PT to a human cell without the inherent problem of pre-existing immunity -
XX
PS Example 14; Page 32; 138pp; English.
XX
CC The present sequence is a primer used in the construction of a gene
CC delivery vehicle comprising an element of adenovirus type 35 or a
CC functional equivalent of such an element. The element is responsible for
CC avoiding or reducing neutralising activity against adenoviral elements by
CC the host to which the gene is to be delivered. The vehicle can be used to
CC deliver genes or nucleic acids of interest to host cells. Use of the
CC delivery system efficiently transfers genetic material to a human cell
CC without the inherent problem of pre-existing immunity, found with
CC previous serotypes.
XX
SQ Sequence 27 BP; 6 A; 11 C; 3 G; 7 T; 0 other;

```
  Query Match             60.8%;  Score 14.6;  DB 22;  Length 27;
  Best Local Similarity   81.0%;  Pred. No. 6.5e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 gtccaaggcagagcaatttct 21
           ||  ||||||| | |||||||
Db      26 GTGGAAGGCAGTGGAATTTCT 6


RESULT   4
AAZ67225
ID   AAZ67225 standard; DNA; 47 BP.
XX
AC   AAZ67225;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:1572.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,G)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 1; Page 565; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 8 A; 12 C; 15 G; 12 T; 0 other;

  Query Match             60.8%;  Score 14.6;  DB 21;  Length 47;
  Best Local Similarity   81.0%;  Pred. No. 7.2e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4 caaggcagagcaatttctgca 24
           || || ||||||  |||||||
Db       4 caggggagagcagcttctgca 24


RESULT   5
AAQ23683
ID   AAQ23683 standard; DNA; 60 BP.
XX
AC   AAQ23683;
XX
DT   01-JUN-1992  (first entry)
XX
DE   PND EEE6405-1.
XX
KW   HIV; PND; principal neutralising determinant; Omp; Neisseria;
KW   outer membrane proteosome; AIDS; vaccine; envelope gene; ss.
XX
OS   Human immunodeficiency virus.
XX
PN   EP471407-A.
XX
PD   19-FEB-1992.
XX
PF   07-AUG-1991;   91EP-0202025.
XX
PR   13-AUG-1990;   90US-0566656.
PR   13-AUG-1990;   90US-0566638.
PR   13-AUG-1990;   90US-0566654.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Lewis JA,  Davide JP,  Waterbury JA;
XX
DR   WPI; 1992-058471/08.
DR   P-PSDB; AAR22956.
XX
PT   New antigenic conjugate of HIV major neutralisation determinant -
PT   covalently linked to outer membrane proteosome of Neisseria,
PT   useful as vaccine and in treating and preventing HIV infections,
PT   AIDS and ARC
XX
PS   Claim 1; Page 172; 177pp; English.
XX
CC   The first 45 bases are missing from the sequence in the specification.
CC   The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78
CC   encode PNDs of HIV (envelope protein) which are useful as immunogens
CC   for AIDS vaccines, partic. in the form of conjugates.
CC   To prepare antigenic conjugates, PND (of HIV) and Omp (of Neisseria)
CC   are prepd. separately, then linked by cross-linking agents, monogeneric
CC   spacers or bigeneric spacers.  The conjugate may comprise 1-50 PNDs.
CC   A PND has 35 amino acids or less, but at least 5, it contains
CC   Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser.
CC   The conjugates as AIDS or HIV vaccines can be used pre- or post-
CC   exposure to prevent or treat HIV infection or disease, and are capable
CC   of producing an immune response specific for the immunogen.
CC   See also AAQ21052-61, AAQ21194-311 and AAQ21321-78.
XX
SQ   Sequence 60 BP; 24 A; 8 C; 16 G; 12 T; 0 other;


  Query Match             60.8%;  Score 14.6;  DB 13;  Length 60;
  Best Local Similarity   81.0%;  Pred. No. 7.5e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4 caaggcagagcaatttctgca 24
           | ||| |||||| ||| ||||
Db       1 ccagggagagcattttatgca 21
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```
RESULT   6
AAX29732
ID   AAX29732 standard; DNA; 44 BP.
XX
AC   AAX29732;
XX
DT   22-JUN-1999  (first entry)
XX
DE   Oligo #3 for scorpion toxin fusion gene.
XX
KW   Toxin; androctonin; scorpion; fusion protein; transgenic plant;
KW   resistance; fungus; bacterium; infection; ss.
XX
OS   Synthetic.
XX
PN   WO9909189-A1.
XX
PD   25-FEB-1999.
XX
PF   18-AUG-1998;   98WO-FR01814.
XX
PR   20-AUG-1997;   97FR-0010632.
XX
PA   (RHON ) RHONE-POULENC AGROCHIMIE.
XX
PI   Derose R,  Freyssinet G,  Hoffmann J;
XX
DR   WPI; 1999-181046/15.
XX
PT   DNA encoding scorpion peptide androctonin - especially for producing
PT   disease-resistant plants
XX
PS   Example 1; Page 12; 37pp; French.
XX
CC   This sequence corresponds to an oligonucleotide used to generate a
CC   fusion gene (AAX29729) comprising the tobacco PR-1alpha gene signal
CC   peptide sequence linked to the gene encoding the toxin androctonin
CC   from the scorpion Androctonus australis, for expression in plants.
CC   Transgenic plants containing androctonin genes are stated to be
CC   resistant to fungal and bacterial infections, especially caused by
CC   Cercospora beticola, Cladosporium herbarum, Fusarium culmorum,
CC   Fusarium graminearum or Phytophthora cinnamomi.
XX
SQ   Sequence 44 BP; 10 A; 7 C; 20 G; 7 T; 0 other;


  Query Match             59.2%;  Score 14.2;  DB 20;  Length 44;
  Best Local Similarity   84.2%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      6 aggcagagcaatttctgca 24
          ||||||| |||  ||||||
Db     13 aggcagatcaagatctgca 31


RESULT   7
AAZ87595/c
ID   AAZ87595 standard; DNA; 50 BP.
XX
AC   AAZ87595;
XX
DT   04-MAY-2000  (first entry)
XX
DE   GM-CSF coding sequence amplifying upstream primer.
XX
KW   CD40; ligand-enhanced cell; LEC; antigen; cytokine-coated cell; CCC;
KW   cytokine; immune response; tumour; pathogen; cytostatic; antimicrobial;
KW   vaccine; GM-CSF; PCR primer; ss.
XX
OS   Mus sp.
XX
PN   WO9961051-A1.
XX
PD   02-DEC-1999.
XX
PF   26-MAY-1999;   99WO-US11609.
XX
PR   26-MAY-1998;   98US-0086780.
PR   02-JUL-1998;   98US-0091525.
XX
PA   (GENI-) GENITRIX LCC.
XX
PI   Segal A;
XX
DR   WPI; 2000-147026/13.
XX
PT   Vaccines comprising antigen-containing cells that are coated with
PT   cytokine or carry CD40 ligand, provide modulated immune response to the
PT   antigen -
XX
PS   Example 3; Page 97; 122pp; English.
XX
CC   The invention provides methods for vaccinating a mammal to a selected
CC   antigen. The method comprises administering a vaccine comprising either
CC   a CD40-ligand-enhanced cell (LEC), containing a specific antigen (Ag)
CC   mixed with an engineered ligand for CD40, or a cytokine-coated cell
CC   (CCC) comprising Ag and mixed with an engineered cytokine, or a LEC or
CC   CCC with an Ag. The methods are used to generate a therapeutic immune
CC   response against tumours or pathogens (bacteria, viruses, fungi or
CC   parasites). The vaccines elicit both cellular and antibody responses and,
CC   compared with use of similar cells that are not CD40 ligand enhanced or
CC   cytokine coated, show a modulated response, i.e. altered efficiency,
CC   rapidity, magnitude or ease of induction. LEC and CCC can be produced
CC   more simply and quickly than cells engineered to express cytokines or
CC   ligands, so allow more rapid treatment, while use of engineered
CC   ligands/cytokines avoids problems of diffusion of soluble proteins away
CC   from the cell (thus also reducing systemic toxicity). Sequences
CC   AAZ87595-96 represent PCR primers for amplifying GM-CSF coding sequence
CC   from mouse lung cDNA library, used in the construction of GM-CSF-GPI, an
CC   engineered cytokine.
XX
SQ   Sequence 50 BP; 9 A; 11 C; 12 G; 18 T; 0 other;


  Query Match             58.3%;  Score 14;  DB 21;  Length 50;
  Best Local Similarity   77.3%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      3 ccaaggcagagcaatttctgca 24
          || ||| | || || |||||||
Db     37 CCCAGGAAAAGTAAATTCTGCA 16


RESULT   8
AAZ04797
ID   AAZ04797 standard; DNA; 20 BP.
XX
AC   AAZ04797;
XX
DT   07-OCT-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW   Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW   paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW   nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW   bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
PN   WO9928475-A2.
XX
PD   10-JUN-1999.
XX
PF   27-NOV-1998;   98WO-IB01939.
```

XX
PR 04-NOV-1998; 98US-0107077.
PR 28-NOV-1997; 97FR-0015041.
PR 17-DEC-1997; 97FR-0016034.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis
XX
PS Disclosure; Page 1718; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal uretritis, epidymitis, cervicitis, salpingitis,
CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
CC and venereal lymphogranulomatosis. The polypeptides of the
CC invention may be of use in treating these diseases.
XX
SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 other;

Query Match 57.5%; Score 13.8; DB 20; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 gcagagcaatttctgca 24
||||||||||||| ||
Db 1 gcagagcaatttcccca 17

RESULT 9
AAV83732
ID AAV83732 standard; DNA; 23 BP.
XX
AC AAV83732;
XX
DT 12-MAR-1999 (first entry)
XX
DE PCR primer L for the uteroglobin gene exon 5 and upstream sequence.
XX
KW Uteroglobin; phospholipase A2; fibronectin; inflammation; asthma;
KW cystic fibrosis; premature labour; infertility; rheumatoid arthritis;
KW type I diabetes; nephropathy; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; pancreatitis; peritonitis; allergy;
KW multiple organ failure; adult respiratory distress syndrome;
KW acute renal failure; organ transplant rejection; autoimmune uveitis;
KW corneal transplant surgery; neonatal RDS; cytomegalovirus retinitis;
KW pneumonia; cystitis; schistosomiasis; vaginal candidiasis; fibrosis;
KW neonatal broncho-pulmonary dysplasia; haemodialysis; glomerulopathy;
KW artificial insemination; PCR primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9853846-A1.
XX
PD 03-DEC-1998.
XX
PF 28-MAY-1998; 98WO-US11026.
XX
PR 28-MAY-1997; 97US-0864357.
XX
PA (CLAR-) CLARAGEN INC.
PA (USSH) US NAT INST OF HEALTH.
XX
PI Mukherjee AB, Pilon AL, Zhang Z;
XX
DR WPI; 1999-059777/05.
XX
PT Treating and preventing inflammation and fibrosis with human
PT uteroglobin - which inhibits phospholipase A2 and binds to
PT fibronectin, for clinical or cosmetic use, e.g. in respiratory
PT distress syndrome
XX
PS Example 3; Page 27; 59pp; English.
XX
CC PCR primers AAV83732-33 were used to amplify exon 5 and its upstream
CC sequence of the murine uteroglobin gene. Recombinant human uteroglobin
CC inhibits phospholipase A2 (PLA2), and binds to fibronectin. Inhibition
CC of PLA2 is used to treat or prevent a wide range of systemic and ocular
CC inflammations, asthma, cystic fibrosis, premature labour, infertility,
CC rheumatoid arthritis, type I diabetes, nephropathy, inflammatory bowel
CC disease, Crohn's disease, ulcerative colitis, pancreatitis, peritonitis,
CC allergy, multiple organ failure, adult respiratory distress syndrome
CC (RDS), acute renal failure, inflammation secondary to infection or
CC surgery, and organ transplant rejection. Some specified applications are
CC in autoimmune uveitis, corneal transplant surgery, neonatal and adult
CC RDS, cytomegalovirus retinitis, pneumonia, cystitis, schistosomiasis and
CC vaginal candidiasis. Fibrotic conditions that can be treated are
CC pulmonary, renal and vascular fibrosis. Uteroglobin may be administered
CC to correct deficiency in endogenous uteroglobin, e.g. in neonatal
CC broncho-pulmonary dysplasia, complications of haemodialysis and
CC inherited glomerulopathy. Uteroglobin can also be used to increase the
CC rate of artificial insemination, in humans or animals, by treatment of
CC sperm, fertilised eggs or embryos before transfer to the uterus.
XX
SQ Sequence 23 BP; 8 A; 5 C; 5 G; 5 T; 0 other;

Query Match 57.5%; Score 13.8; DB 20; Length 23;
Best Local Similarity 88.2%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 tccaaggcagagcaatt 18
|||||||||||| || ||
Db 2 tccaaggcagaacattt 18

RESULT 10
AAC65579
ID AAC65579 standard; DNA; 23 BP.
XX
AC AAC65579;
XX
DT 14-FEB-2001 (first entry)
XX
DE Uteroglobin knockout mouse PCR primer L.
XX
KW Mouse; uteroglobin; immunoglobulin A mediated disease; IgA nephropathy;
KW autoimmune disorder; pulmonary inflammation; Wegener's granulomatosus;
KW Goodpasture's disease; diabetic glomerulosclerosis; PCR primer; ss.
XX
OS Mus sp.
XX
PN WO200062795-A2.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US09979.
XX
PR 21-APR-1999; 99US-0130434.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Mukherjee AB, Zheng F, Zhang Z;
XX

DR WPI; 2000-687100/67.
XX
PT Use of a composition comprising uteroglobin (or a fragment, derivative,
PT mimetic or variant), for inhibiting or treating an immunoglobulin-A
PT mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
PT pulmonary inflammation -
XX
PS Example 1; Page 19; 60pp; English.
XX
CC The present invention describes the use of uteroglobin in the diagnosis
CC and prevention of IgA mediated diseases, such as IgA nephropathy,
CC Wegener's granulomatosus, Goodpasture's disease and diabetic
CC glomerulosclerosis. This is possible as uteroglobin binds to fibronectin,
CC preventing the complexing of fibronectin with IgA and the deposition of
CC immune complexes in the kidney.
XX
SQ Sequence 23 BP; 8 A; 5 C; 5 G; 5 T; 0 other;

Query Match 57.5%; Score 13.8; DB 21; Length 23;
Best Local Similarity 88.2%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 tccaaggcagagcaatt 18
||||||||||| || ||
Db 2 tccaaggcagaacattt 18

RESULT 11
AAZ58235
ID AAZ58235 standard; DNA; 23 BP.
XX
AC AAZ58235;
XX
DT 08-MAY-2000 (first entry)
XX
DE Mouse uteroglobin gene exon 2 region PCR primer L.
XX
KW Uteroglobin; knockout mouse; inflammation; antiinflammatory;
KW cancer; tumour; metastasis; haematopoiesis; therapy; PCR primer;
KW ss.
XX
OS Mus musculus.
XX
PN WO200004863-A2.
XX
PD 03-FEB-2000.
XX
PF 19-JUL-1999; 99WO-US16312.
XX
PR 21-JUL-1998; 98US-0120264.
XX
PA (CLAR-) CLARAGEN INC.
PA (USSH) US NAT INST OF HEALTH.
XX
PI Pilon A, Mukherjee AB, Zhang Z;
XX
DR WPI; 2000-182512/16.
XX
PT Treating and preventing primary cancer cell growth or tumor metastasis
PT and stimulating hematopoiesis -
XX
PS Example 3; Page 29; 73pp; English.
XX
CC The present sequence is that of primer L, designed from intron 1
CC of the mouse uteroglobin (UG) gene. It was used with primer R (see
CC AAZ58236) in the PCR amplification of a 0.9 kb fragment containing
CC part of UG exon 2 and its upstream sequence. The primers introduce
CC NotI and XhoI sites into the termini of the PCR product for
CC directional subcloning into a vector designed to target and
CC interrupt the endogenous murine UG gene. The vector was used in
CC the creation of a transgenic UG knockout mouse for the purpose of
CC determining the role of UG in mammalian physiology and to generate
CC a model for UG as a therapeutic in several inflammatory clinical
CC conditions. The invention provides compositions and methods for
CC preventing and treating primary cancer cell growth and tumour
CC metastasis, as well as stimulation of haematopoiesis, by targeting
CC a UG receptor with recombinant human UG.
XX
SQ Sequence 23 BP; 8 A; 5 C; 5 G; 5 T; 0 other;

Query Match 57.5%; Score 13.8; DB 21; Length 23;
Best Local Similarity 88.2%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 tccaaggcagagcaatt 18
||||||||||| || ||
Db 2 tccaaggcagaacattt 18

RESULT 12
AAX32801
ID AAX32801 standard; DNA; 26 BP.
XX
AC AAX32801;
XX
DT 25-JUN-1999 (first entry)
XX
DE Human mpl ligand analogues synthesising primer N36(2)-F.
XX
KW mpl ligand; analogue; N-linked glycosylation site; megakaryocyte;
KW platelet deficiency; thrombocytopenia; aplastic anemia; tumour; human;
KW systemic lupus erythematosus; splenomegaly; Fanconi's syndrome; primer;
KW vitamin B12 deficiency; folic acid deficiency; May-Hegglin anomaly;
KW Wiskott-Aldrich syndrome; paroxysmal nocturnal hemoglobinuria; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9913076-A1.
XX
PD 18-MAR-1999.
XX
PF 09-SEP-1998; 98WO-US18753.
XX
PR 11-SEP-1997; 97US-0927855.
XX
PA (AMGE-) AMGEN INC.
XX
PI Elliott SG;
XX
DR WPI; 1999-243730/20.
XX
PT Mpl ligand analogue for treatment of thrombocytopaenia
XX
PS Example 14; Page 47; 74pp; English.
XX
CC The invention relates to analogues of human mpl ligand, which comprise
CC one more changed N-linked glycosylation site, selected from (Asn164),
CC (Asn163) and (Asn30, Thr32, Asn56, Asn120, Thr122, Asn164) of the native
CC mpl sequence. The mpl analogue can be used to treat conditions which
CC involve megakaryocyte/platelet deficiency. The analogue can especially
CC be used to treat thrombocytopenia. Diseases that involve
CC thrombocytopenia that can be treated include aplastic anemia, idiopathic
CC thrombocytopenia, metastatic tumours which result in thrombocytopenia,
CC systemic lupus erythematosus, splenomegaly, Fanconi's syndrome, vitamin
CC B12 deficiency, folic acid deficiency, May-Hegglin anomaly,
CC Wiskott-Aldrich syndrome and paroxysmal nocturnal hemoglobinuria.
CC Sequences AAX32768-806 represent primers used for synthesising mpl
CC analogues N16 to N40.
XX
SQ Sequence 26 BP; 8 A; 7 C; 8 G; 3 T; 0 other;

Query Match 56.7%; Score 13.6; DB 20; Length 26;

```
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      3 ccaaggcagagcaatttctg 22
          |||||||| || |  |||||
Db      3 ccaaggcacaggacattctg 22


RESULT  13
AAX32802/c
ID   AAX32802 standard; DNA; 26 BP.
XX
AC   AAX32802;
XX
DT   25-JUN-1999  (first entry)
XX
DE   Human mpl ligand analogues synthesising primer N36(2)-R.
XX
KW   mpl ligand; analogue; N-linked glycosylation site; megakaryocyte;
KW   platelet deficiency; thrombocytopenia; aplastic anemia; tumour; human;
KW   systemic lupus erythematosus; splenomegaly; Fanconi's syndrome; primer;
KW   vitamin B12 deficiency; folic acid deficiency; May-Hegglin anomaly;
KW   Wiskott-Aldrich syndrome; paroxysmal nocturnal hemoglobinuria; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9913076-A1.
XX
PD   18-MAR-1999.
XX
PF   09-SEP-1998;   98WO-US18753.
XX
PR   11-SEP-1997;   97US-0927855.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Elliott SG;
XX
DR   WPI; 1999-243730/20.
XX
PT   Mpl ligand analogue for treatment of thrombocytopaenia
XX
PS   Example 14; Page 47; 74pp; English.
XX
CC   The invention relates to analogues of human mpl ligand, which comprise
CC   one more changed N-linked glycosylation site, selected from (Asn164),
CC   (Asn163) and (Asn30, Thr32, Asn56, Asn120, Thr122, Asn164) of the native
CC   mpl sequence. The mpl analogue can be used to treat conditions which
CC   involve megakaryocyte/platelet deficiency. The analogue can especially
CC   be used to treat thrombocytopenia. Diseases that involve
CC   thrombocytopenia that can be treated include aplastic anemia, idiopathic
CC   thrombocytopenia, metastatic tumours which result in thrombocytopenia,
CC   systemic lupus erythematosus, splenomegaly, Fanconi's syndrome, vitamin
CC   B12 deficiency, folic acid deficiency, May-Hegglin anomaly,
CC   Wiskott-Aldrich syndrome and paroxysmal nocturnal hemoglobinuria.
CC   Sequences AAX32768-806 represent primers used for synthesising mpl
CC   analogues N16 to N40.
XX
SQ   Sequence 26 BP; 3 A; 8 C; 7 G; 8 T; 0 other;


  Query Match             56.7%;  Score 13.6;  DB 20;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      3 ccaaggcagagcaatttctg 22
          |||||||| || |  |||||
Db     24 CCAAGGCACAGGACATTCTG 5


RESULT  14
AAZ69023
ID   AAZ69023 standard; DNA; 47 BP.
XX
AC   AAZ69023;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:3379.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,A)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 3; Page 951; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 10 A; 18 C; 10 G; 9 T; 0 other;


  Query Match             56.7%;  Score 13.6;  DB 21;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 gtccaaggcagagcaatttc 20
          |||||  |||| || |||||
Db     24 gtccagagcagcgccatttc 43


RESULT  15
AAA53746/c
ID   AAA53746 standard; DNA; 48 BP.
XX
```

AC AAA53746;
XX
DT 19-DEC-2000 (first entry)
XX
DE Str1 promoter RV region sequence.
XX
KW AP2; transcription factor; plant metabolism; metabolite; primary;
KW secondary; alkaloid; terpenoid indole alkaloid; TIA; pharmaceutical;
KW food colouring; flavouring; fragrance; antimicrobial; pathogenic;
KW insecticide; gene expression; modulation; ds.
XX
OS Catharanthus roseus.
XX
PN WO200046383-A2.
XX
PD 10-AUG-2000.
XX
PF 07-FEB-2000; 2000WO-NL00075.
XX
PR 05-FEB-1999; 99DK-0000158.
PR 10-FEB-1999; 99US-0119388.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Memelink J, Van Der Fits CTE, Menke FLH, Kijne JW;
XX
DR WPI; 2000-499380/44.
XX
PT Modulating level of metabolites and stress resistance in recombinant
PT cells for synthesis of plant metabolites such as alkaloids including
PT terpenoid indole alkaloids, by providing transcription factor to the
PT cell
XX
PS Example 6; Page 66; 101pp; English.
XX
CC Many plant secondary metabolites have value as pharmaceuticals,
CC food colourings, flavours and fragrances. Some plant secondary
CC metabolites are linked to plant or plant cell defence mechanisms
CC and may confer to the plant antimicrobial activity, protection
CC against UV light, herbivores, pathogens, insects and nematodes.
CC Plant secondary metabolites such as terpenoid indole alkaloids
CC (TIA) represent a class of pharmaceutically useful compounds which
CC naturally occur in many plant species. New methods are described
CC which modulate the expression of one or more genes involved in the
CC biosynthesis of plant metabolites or their precursors in plant cells.
CC The method comprises inserting into a plant cell a sequence encoding
CC a transcription factor comprising an AP2 DNA-binding domain and by
CC modifying the expression of that transcription factor. Transcription
CC factors comprising an AP2 DNA-binding domain are useful as central
CC regulators of complex metabolite pathways involving numerous target
CC genes for such transcription factors. This means that the yield of
CC commercially valuable metabolite compounds can be enhanced and the
CC tolerance of plants towards exogenous stress factors can be
CC influenced. The method is useful for modulating the level of one or
CC more metabolites. By providing a transcription factor to the cell the
CC level of the metabolite is enhanced by at least 10%, 25% or 100% or
CC reduced 10%, 25%, 50% or 90% relative to a cell to which the
CC transcription factor is not provided. The RV region of the Str1
CC promoter has been identified as an elicitor- and jasmonate-responsive
CC element. The sequence was block mutated using primers (See
CC AAA53747-A53754) to identify the Octadecanoid Responsive Catharanthus
CC AP2-domain protein (ORCA) -1 and -2 binding site within the Str1 RV
CC region since they are transcriptional activators of the Str1 promoter in
CC C. roseus cells.
XX
SQ Sequence 48 BP; 10 A; 14 C; 8 G; 16 T; 0 other;

Query Match 56.7%; Score 13.6; DB 21; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gtccaaggcagagcaatttc 20
|||||||| | | || ||||
Db 47 GTCCAAGGGAAATCACTTTC 28

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